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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/084,837B

DATE: 10/22/2003

TIME: 10:31:51

Input Set : A:\1997-269.ST25.txt

Output Set: N:\CRF4\10222003\I084837B.raw

3 <110> APPLICANT: AKZO Nobel NV  
 5 <120> TITLE OF INVENTION: recombinant birnavirus vaccine  
 7 <130> FILE REFERENCE: 1997-269-US  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/084,837B  
 C--> 9 <141> CURRENT FILING DATE: 1998-05-26  
 9 <150> PRIOR APPLICATION NUMBER: EP 97201599.4  
 10 <151> PRIOR FILING DATE: 1997-05-26  
 12 <160> NUMBER OF SEQ ID NOS: 13  
 14 <170> SOFTWARE: PatentIn version 3.2  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 2827  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Infectious bursal disease virus  
 22 <220> FEATURE:  
 23 <221> NAME/KEY: CDS  
 24 <222> LOCATION: (112)..(2745)  
 26 <400> SEQUENCE: 1  
 27 ggatac gatg ggtctgaccc tctgggagtc acgaattaac gtggctacta ggggcgatac 60  
 29 ccgccgctgg ccgccacggt agtggctcct cttcttgatg attctgccac c atg agt 117  
 30 Met Ser  
 31 1  
 33 gac att ttc aac agt cca cag gcg cga agc acg atc tca gca gcg ttc 165  
 34 Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala Ala Phe  
 35 5 10 15  
 37 ggc ata aag cct act gct gga caa gac gtg gaa gaa ctc ttg atc cct 213  
 38 Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu Ile Pro  
 39 20 25 30  
 41 aaa gtt tgg gtg cca cct gag gat ccg ctt gcc agc cct agt cga ctg 261  
 42 Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser Arg Leu  
 43 35 40 45 50  
 45 gca aag ttc ctc aga gag aac ggc tac aaa gtt ttg cag cca cgg tct 309  
 46 Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro Arg Ser  
 47 55 60 65  
 49 ctg ccc gag aat gag gag tat gag acc gac caa ata ctc cca gac tta 357  
 50 Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro Asp Leu  
 51 70 75 80  
 53 gca tgg atg cga cag ata gaa ggg gct gtt tta aaa ccc act cta tct 405  
 54 Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr Leu Ser  
 55 85 90 95  
 57 ctc cct att gga gat cag gag tac ttc cca aag tac tac cca aca cat 453  
 58 Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro Thr His  
 59 100 105 110  
 62 cgc cct agc aag gag aag ccc aat gcg tac ccg cca gac atc gca cta 501

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63	Arg	Pro	Ser	Lys	Glu	Lys	Pro	Asn	Ala	Tyr	Pro	Pro	Asp	Ile	Ala	Leu	
64	115					120					125					130	
66	ctc	aag	cag	atg	att	tac	ctg	ttt	ctc	cag	gtt	cca	gag	gcc	aac	gag	549
67	Leu	Lys	Gln	Met	Ile	Tyr	Leu	Phe	Leu	Gln	Val	Pro	Glu	Ala	Asn	Glu	
68				135					140					145			
70	ggc	cta	aag	gat	gaa	gta	acc	ctc	ttg	acc	caa	aac	ata	agg	gac	aag	597
71	Gly	Leu	Lys	Asp	Glu	Val	Thr	Leu	Leu	Thr	Gln	Asn	Ile	Arg	Asp	Lys	
72			150					155					160				
74	gcc	tat	gga	agt	ggg	acc	tac	atg	gga	caa	gca	aat	cga	ctt	gtg	gcc	645
75	Ala	Tyr	Gly	Ser	Gly	Thr	Tyr	Met	Gly	Gln	Ala	Asn	Arg	Leu	Val	Ala	
76			165					170					175				
78	atg	aag	gag	gtc	gcc	act	gga	aga	aac	cca	aac	aag	gat	cct	cta	aag	693
79	Met	Lys	Glu	Val	Ala	Thr	Gly	Arg	Asn	Pro	Asn	Lys	Asp	Pro	Leu	Lys	
80	180					185				190							
82	ctt	ggg	tac	act	ttt	gag	agc	atc	gcg	cag	cta	ctt	gac	atc	aca	cta	741
83	Leu	Gly	Tyr	Thr	Phe	Glu	Ser	Ile	Ala	Gln	Leu	Leu	Asp	Ile	Thr	Leu	
84	195			200					205				210				
86	ccg	gta	ggc	cca	ccc	ggt	gag	gat	gac	aag	ccc	tgg	gtg	cca	ctc	aca	789
87	Pro	Val	Gly	Pro	Pro	Gly	Glu	Asp	Asp	Lys	Pro	Trp	Val	Pro	Leu	Thr	
88			215					220				225					
90	aga	gtg	ccg	tca	cgg	atg	ttg	gtg	ctg	acg	gga	gac	gta	gat	ggc	gac	837
91	Arg	Val	Pro	Ser	Arg	Met	Leu	Val	Leu	Thr	Gly	Asp	Val	Asp	Gly	Asp	
92			230					235				240					
94	ttt	gag	gtt	gaa	gat	tac	ctt	ccc	aaa	atc	aac	ctc	aag	tca	tca	agt	885
95	Phe	Glu	Val	Glu	Asp	Tyr	Leu	Pro	Lys	Ile	Asn	Leu	Lys	Ser	Ser	Ser	
96			245				250					255					
98	gga	cta	cca	tat	gta	ggt	cgc	acc	aaa	gga	gag	aca	att	ggc	gag	atg	933
99	Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly	Glu	Met	
100	260					265				270							
102	ata	gct	atc	tca	aac	cag	ttt	ctc	aga	gag	cta	tca	aca	ctg	ttg	aag	981
103	Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Thr	Leu	Leu	Lys	
104	275			280					285				290				
106	caa	ggt	gca	ggg	aca	aag	ggg	tca	aac	aag	aag	aag	cta	ctc	agc	atg	1029
107	Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu	Ser	Met	
108			295					300				305					
110	tta	agt	gac	tat	tgg	tac	tta	tca	tgc	ggg	ctt	ttg	ttt	cca	aag	gct	1077
111	Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro	Lys	Ala	
112			310					315				320					
114	gaa	agg	tac	gac	aaa	agt	aca	tgg	ctc	acc	aag	acc	cgg	aac	ata	tgg	1125
115	Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn	Ile	Trp	
116			325					330				335					
118	tca	gct	cca	tcc	cca	aca	cac	ctc	atg	atc	tct	atg	atc	acc	tgg	ccc	1173
119	Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr	Trp	Pro	
120	340					345						350					
123	gtg	atg	tcc	aac	agc	cca	aat	aac	gtg	ttg	aac	att	gaa	ggg	tgt	cca	1221
124	Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly	Cys	Pro	
125	355			360				365				370					
127	tca	ctc	tac	aaa	ttc	aac	ccg	ttc	aga	gga	ggg	ttg	aac	agg	atc	gtc	1269
128	Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg	Ile	Val	

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129		375		380		385	
131	gag tgg ata ttg gcc ccg gaa gaa ccc aag gct ctt gta tat gcg gac						1317
132	Glu Trp Ile Leu Ala Pro Glu Glu Pro Lys Ala Leu Val Tyr Ala Asp						
133		390		395		400	
135	aac ata tac att gtc cac tca aac acg tgg tac tca att gac cta gag						1365
136	Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp Leu Glu						
137		405		410		415	
139	aag ggt gag gca aac tgc act cgc caa cac atg caa gcc gca atg tac						1413
140	Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala Met Tyr						
141		420		425		430	
143	tac ata ctc acc aga ggg tgg tca gac aac ggc gac cca atg ttc aat						1461
144	Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met Phe Asn						
145	435		440		445	450	
147	caa aca tgg gcc acc ttt gcc atg aac att gcc cct gct cta gtg gtg						1509
148	Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu Val Val						
149		455		460		465	
151	gac tca tcg tgc ctg ata atg aac ctg caa att aag acc tat ggt caa						1557
152	Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr Gly Gln						
153		470		475		480	
155	ggc agc ggg aat gca gcc acg ttc atc aac aac cac ctc ttg agc aca						1605
156	Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu Ser Thr						
157		485		490		495	
159	cta gtg ctt gac cag tgg aac ctg atg aga cag ccc aga cca gac agc						1653
160	Leu Val Leu Asp Gln Trp Asn Leu Met Arg Gln Pro Arg Pro Asp Ser						
161		500		505		510	
163	gag gag ttc aaa tca att gag gac aag cta ggt atc aac ttt aag att						1701
164	Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe Lys Ile						
165	515		520		525	530	
167	gag agg tcc att gat gat atc agg ggc aag ctg aga cag ctt gtc ctc						1749
168	Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu Val Leu						
169		535		540		545	
171	ctt gca caa cca ggg tac ctg agt ggg ggg gtt gaa cca gaa caa tcc						1797
172	Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu Gln Ser						
173		550		555		560	
175	agc cca act gtt gag ctt gac cta cta ggg tgg tca gct aca tac agc						1845
176	Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr Tyr Ser						
177		565		570		575	
179	aaa gat ctc ggg atc tat gtg ccg gtg ctt gac aag gaa cgc cta ttt						1893
180	Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg Leu Phe						
181		580		585		590	
184	tgt tct gct gcg tat ccc aag gga gta gag aac aag agt ctc aag tcc						1941
185	Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu Lys Ser						
186	595		600		605	610	
188	aaa gtc ggg atc gag cag gca tac aag gta gtc agg tat gag gcg ttg						1989
189	Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu Ala Leu						
190		615		620		625	
192	agg ttg gta ggt ggt tgg aac tac cca ctc ctg aac aaa gcc tgc aag						2037
193	Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala Cys Lys						
194		630		635		640	

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```

196 aat aac gca ggc gcc gct cgg cgg cat ctg gag gcc aag ggg ttc cca      2085
197 Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly Phe Pro
198      645      650      655
200 ctc gac gag ttc cta gcc gag tgg tct gag ctg tca gag ttc ggt gag      2133
201 Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe Gly Glu
202      660      665      670
204 gcc ttc gaa ggc ttc aat atc aag ctg acc gta aca tct gag agc cta      2181
205 Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu Ser Leu
206 675      680      685      690
208 gcc gaa ctg aac aag cca gta ccc ccc aag ccc cca aat gtc aac aga      2229
209 Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val Asn Arg
210      695      700      705
212 cca gtc aac act ggg gga ctc aag gca gtc agc aac gcc ctc aag acc      2277
213 Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu Lys Thr
214      710      715      720
216 ggt cgg tac agg aac gaa gcc gga ctg agt ggt ctc gtc ctt cta gcc      2325
217 Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu Leu Ala
218      725      730      735
220 aca gca aga agc cgt ctg caa gat gca gtt aag gcc aag gca gaa gcc      2373
221 Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala Glu Ala
222      740      745      750
224 gag aaa ctc cac aag tcc aag cca gac gac ccc gat gca gac tgg ttc      2421
225 Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp Trp Phe
226 755      760      765      770
228 gaa aga tca gaa act ctg tca gac ctt ctg gag aaa gcc gac atc gcc      2469
229 Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp Ile Ala
230      775      780      785
232 agc aag gtc gcc cac tca gca ctc gtg gaa aca agc gac gcc ctt gaa      2517
233 Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala Leu Glu
234      790      795      800
236 gca gtt cag tcg act tcc gtg tac acc ccc aag tac cca gaa gtc aag      2565
237 Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu Val Lys
238      805      810      815
240 aac cca cag acc gcc tcc aac ccc gtt gtt ggg ctc cac ctg ccc gcc      2613
241 Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu Pro Ala
242      820      825      830
245 aag aga gcc acc ggt gtc cag gcc gct ctt ctc gga gca gga acg agc      2661
246 Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly Thr Ser
247 835      840      845      850
249 aga cca atg ggg atg gag gcc cca aca cgg tcc aag aac gcc gtg aaa      2709
250 Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala Val Lys
251      855      860      865
253 atg gcc aaa cgg cgg caa cgc caa aag gag agc cgc taacagccat      2755
254 Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg
255      870      875
257 gatgggaacc actcaagaag aggacactaa tcccagaccc cgtatccccg gccttcgcct      2815
259 gcggggggccc cc      2827
262 <210> SEQ ID NO: 2
263 <211> LENGTH: 878

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264 &lt;212&gt; TYPE: PRT

265 &lt;213&gt; ORGANISM: Infectious bursal disease virus

267 &lt;400&gt; SEQUENCE: 2

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269 Met Ser Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala
270 1 5 10 15
273 Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
274 20 25 30
277 Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser
278 35 40 45
281 Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro
282 50 55 60
285 Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
286 65 70 75 80
289 Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
290 85 90 95
293 Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
294 100 105 110
297 Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
298 115 120 125
301 Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
302 130 135 140
306 Asn Glu Gly Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
307 145 150 155 160
310 Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Asn Arg Leu
311 165 170 175
314 Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro
315 180 185 190
318 Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile
319 195 200 205
322 Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro
323 210 215 220
326 Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp
327 225 230 235 240
330 Gly Asp Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser
331 245 250 255
334 Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly
335 260 265 270
338 Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Thr Leu
339 275 280 285
342 Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu
343 290 295 300
346 Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro
347 305 310 315 320
350 Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn
351 325 330 335
354 Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr
355 340 345 350
358 Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly
359 355 360 365

```

RAW SEQUENCE LISTING ERROR SUMMARY  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:9,10,11,12,13

**VERIFICATION SUMMARY**

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Input Set : A:\1997-269.ST25.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date